

# SEQUENCE LISTING

<110> Young, John A.T.  
Bradley, Kenneth A.  
Collier, Robert J.  
Mogridge, Jeremy S.

<120> Anthrax Toxin Receptor

<130> 960296.97745

<140>

<141>

<150> 60/251,481

<151> 2000-12-05

<160> 10

<170> PatentIn Ver. 2.1

<210> 1

<211> 1414

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (104)..(1207)

<400> 1

aggaccgcg aggaagggcc cgcggatggc gcgtccctga gggtcgtggc gagttcgcgg 60

agcgtgggaa ggagcggacc ctgctctccc cgggctgogg gcc atg gcc acg gcg 115  
Met Ala Thr Ala

1

gag cgg aga gcc ctc ggc atc ggc ttc cag tgg ctc tct ttg gcc act 163  
Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr  
5 10 15 20

ctg gtg ctc atc tgc gcc ggg caa ggg gga cgc agg gag gat ggg ggt 211  
Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly  
25 30 35

cca gcc tgc tac ggc gga ttt gac ctg tac ttc att ttg gac aaa tca 259  
Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser  
40 45 50

gga agt gtg ctg cac cac tgg aat gaa atc tat tac ttt gtg gaa cag 307  
Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln  
55 60 65

ttg gct cac aaa ttc atc agc cca cag ttg aga atg tcc ttt att gtt 355  
Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met Ser Phe Ile Val  
70 75 80

ttc tcc acc cga gga aca acc tta atg aaa ctg aca gaa gac aga gaa	403
Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp Arg Glu	
85 90 95 100	
caa atc cgt caa ggc cta gaa gaa ctc cag aaa gtt ctg cca gga gga	451
Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro Gly Gly	
105 110 115	
gac act tac atg cat gaa gga ttt gaa agg gcc agt gag cag att tat	499
Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr	
120 125 130	
tat gaa aac aga caa ggg tac agg aca gcc agc gtc atc att gct ttg	547
Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu	
135 140 145	
act gat gga gaa ctc cat gaa gat ctc ttt ttc tat tca gag agg gag	595
Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu	
150 155 160	
gct aat agg tct cga gat ctt ggt gca att gtt tac tgt gtt ggt gtg	643
Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val Gly Val	
165 170 175 180	
aaa gat ttc aat gag aca cag ctg gcc cgg att gcg gac agt aag gat	691
Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp	
185 190 195	
cat gtg ttt ccc gtg aat gac ggc ttt cag gct ctg caa ggc atc atc	739
His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile	
200 205 210	
cac tca att ttg aag aag tcc tgc atc gaa att cta gca gct gaa cca	787
His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro	
215 220 225	
tcc acc ata tgt gca gga gag tca ttt caa gtt gtc gtg aga gga aac	835
Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg Gly Asn	
230 235 240	
ggc ttc cga cat gcc cgc aac gtg gac agg gtc ctc tgc agc ttc aag	883
Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser Phe Lys	
245 250 255 260	
atc aat gac tcg gtc aca ctc aat gag aag ccc ttt tct gtg gaa gac	931
Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ser Val Glu Asp	
265 270 275	
act tat tta ctg tgt cca gcg cct atc tta aaa gaa gtt ggc atg aaa	979
Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly Met Lys	
280 285 290	
gct gca ctc cag gtc agc atg aac gat ggc ctc tct ttt atc tcc agt	1027
Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile Ser Ser	
295 300 305	

tct gtc atc atc acc acc aca cac tgt tct gac ggt tcc atc ctg gcc 1075  
Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly Ser Ile Leu Ala  
310 315 320  
  
atc gcc ctg ctg atc ctg ttc ctg ctc cta gcc ctg gct ctc ctc tgg 1123  
Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu Ala Leu Leu Trp  
325 330 335 340  
  
tgg ttc tgg ccc ctc tgc tgc act gtg att atc aag gag gtc cct cca 1171  
Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys Glu Val Pro Pro  
345 350 355  
  
ccc cct gcc gag gag agt gag gaa aat aaa ata aaa taacaagaag 1217  
Pro Pro Ala Glu Glu Ser Glu Glu Asn Lys Ile Lys  
360 365  
  
aagaaagaaa gaaatccac agaaacagat aacctaacac agcccgtgca acgtatttta 1277  
  
tacaatgctc tgaaaatcat agtctcaatc tagacagtct tttcctctag ttcctgtat 1337  
  
tcaaattcca gtgtctaaca ttcaataaat agctatatga aatcaaaaaa aaaaaaaaaa 1397  
  
aaaaaaaaa aaaaaaa 1414

<210> 2  
<211> 368  
<212> PRT  
<213> Homo sapiens

<400> 2  
Met Ala Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu  
1 5 10 15  
  
Ser Leu Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg  
20 25 30  
  
Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile  
35 40 45  
  
Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr  
50 55 60  
  
Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met  
65 70 75 80  
  
Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr  
85 90 95  
  
Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val  
100 105 110  
  
Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser  
115 120 125  
  
Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val  
130 135 140

```

Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr
145                      150                      155                      160

Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr
                      165                      170                      175

Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala
                      180                      185                      190

Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu
                      195                      200                      205

Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu
                      210                      215                      220

Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val
225                      230                      235                      240

Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu
                      245                      250                      255

Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe
                      260                      265                      270

Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu
                      275                      280                      285

Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser
                      290                      295                      300

Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Asp Gly
305                      310                      315                      320

Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu Phe Leu Leu Leu Ala Leu
                      325                      330                      335

Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys Cys Thr Val Ile Ile Lys
                      340                      345                      350

Glu Val Pro Pro Pro Pro Ala Glu Glu Ser Glu Glu Asn Lys Ile Lys
                      355                      360                      365

```

```

<210> 3
<211> 180
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: von Willebrand
      factor A domain consensus sequence

```

```

<400> 3
Pro Leu Asp Val Val Phe Leu Leu Asp Gly Ser Gly Ser Met Gly Gly
 1              5              10              15

```

Asn Arg Phe Glu Leu Ala Lys Glu Phe Val Leu Lys Leu Val Glu Gln  
                   20                                  25                                  30  
 Leu Asp Ile Gly Pro Arg Gly Asp Arg Val Gly Leu Val Thr Phe Ser  
                   35                                  40                                  45  
 Ser Asp Ala Arg Val Leu Phe Pro Leu Asn Asp Ser Gln Ser Lys Asp  
                   50                                  55                                  60  
 Ala Leu Leu Glu Ala Leu Ala Asn Leu Ser Tyr Ser Leu Gly Gly Gly  
                   65                                  70                                  75                                  80  
 Thr Asn Leu Gly Ala Ala Leu Glu Tyr Ala Leu Glu Asn Leu Phe Ser  
                                   85                                  90                                  95  
 Glu Ser Ala Gly Ser Arg Arg Gly Ala Pro Lys Val Leu Ile Leu Ile  
                   100                                  105                                  110  
 Thr Asp Gly Glu Ser Asn Asp Gly Gly Glu Asp Ile Leu Lys Ala Ala  
                   115                                  120                                  125  
 Lys Glu Leu Lys Arg Ser Gly Val Lys Val Phe Val Val Gly Val Gly  
                   130                                  135                                  140  
 Asn Ala Val Asp Glu Glu Glu Leu Lys Lys Leu Ala Ser Ala Pro Gly  
                   145                                  150                                  155                                  160  
 Gly Val Phe Ala Val Glu Asp Leu Pro Glu Leu Leu Asp Leu Leu Ile  
                                   165                                  170                                  175  
 Asp Leu Leu Leu  
                   180

<210> 4  
 <211> 198  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Cys Pro Ser Leu Ile Asp Val Val Val Val Cys Asp Glu Ser Asn Ser  
           1                                  5                                  10                                  15  
 Ile Tyr Pro Trp Asp Ala Val Lys Asn Phe Leu Glu Lys Phe Val Gln  
                   20                                  25                                  30  
 Gly Leu Asp Ile Gly Pro Thr Lys Thr Gln Val Gly Leu Ile Gln Tyr  
                   35                                  40                                  45  
 Ala Asn Asn Pro Arg Val Val Phe Asn Leu Asn Thr Tyr Lys Thr Lys  
                   50                                  55                                  60  
 Glu Glu Met Ile Val Ala Thr Ser Gln Thr Ser Gln Tyr Gly Gly Asp  
                   65                                  70                                  75                                  80

Leu Thr Asn Thr Phe Gly Ala Ile Gln Tyr Ala Arg Lys Tyr Ala Tyr  
                     85                    90                    95  
 Ser Ala Ser Gly Gly Arg Arg Ser Ala Ala Thr Lys Val Met Val Val  
                     100                    105                    110  
 Val Thr Asp Gly Glu Ser His Asp Gly Ser Met Leu Lys Ala Val Ile  
                     115                    120                    125  
 Asp Gln Cys Asn His Asp Asn Ile Leu Arg Phe Gly Ile Ala Val Leu  
                     130                    135                    140  
 Gly Tyr Leu Asn Arg Asn Ala Leu Asp Thr Lys Asn Leu Ile Lys Glu  
 145                    150                    155                    160  
 Ile Lys Ala Ile Ala Ser Ile Pro Thr Glu Arg Tyr Phe Phe Asn Val  
                     165                    170                    175  
 Ser Asp Glu Ala Ala Leu Leu Glu Lys Ala Gly Thr Leu Gly Glu Gln  
                     180                    185                    190  
 Ile Phe Ser Ile Glu Gly  
                     195

<210> 5  
 <211> 5540  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (144) .. (1835)

<400> 5  
 aattgcttcc ggggagttgc gagggagcga gggggaataa aggaccgcgc aggaagggcc 60  
 cgcggtatggc gcgtccctga gggtcgtggc gagttcgcgc agcgtgggaa ggagcggacc 120  
 ctgctctccc cgggctgcgc gcc atg gcc acg gcg gag cgg aga gcc ctc ggc 173  
                     Met Ala Thr Ala Glu Arg Arg Ala Leu Gly  
                                     1                                    5                                    10  
 atc ggc ttc cag tgg ctc tct ttg gcc act ctg gtg ctc atc tgc gcc 221  
 Ile Gly Phe Gln Trp Leu Ser Leu Ala Thr Leu Val Leu Ile Cys Ala  
                     15                    20                    25  
 ggg caa ggg gga cgc agg gag gat ggg ggt cca gcc tgc tac ggc gga 269  
 Gly Gln Gly Gly Arg Arg Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly  
                     30                    35                    40  
 ttt gac ctg tac ttc att ttg gac aaa tca gga agt gtg ctg cac cac 317  
 Phe Asp Leu Tyr Phe Ile Leu Asp Lys Ser Gly Ser Val Leu His His  
                     45                    50                    55

tgg aat gaa atc tat tac ttt gtg gaa cag ttg gct cac aaa ttc atc	365
Trp Asn Glu Ile Tyr Tyr Phe Val Glu Gln Leu Ala His Lys Phe Ile	
60 65 70	
agc cca cag ttg aga atg tcc ttt att gtt ttc tcc acc cga gga aca	413
Ser Pro Gln Leu Arg Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr	
75 80 85 90	
acc tta atg aaa ctg aca gaa gac aga gaa caa atc cgt caa ggc cta	461
Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu	
95 100 105	
gaa gaa ctc cag aaa gtt ctg cca gga gga gac act tac atg cat gaa	509
Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu	
110 115 120	
gga ttt gaa agg gcc agt gag cag att tat tat gaa aac aga caa ggg	557
Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly	
125 130 135	
tac agg aca gcc agc gtc atc att gct ttg act gat gga gaa ctc cat	605
Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu His	
140 145 150	
gaa gat ctc ttt ttc tat tca gag agg gag gct aat agg tct cga gat	653
Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp	
155 160 165 170	
ctt ggt gca att gtt tac tgt gtt ggt gtg aaa gat ttc aat gag aca	701
Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr	
175 180 185	
cag ctg gcc cgg att gcg gac agt aag gat cat gtg ttt ccc gtg aat	749
Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His Val Phe Pro Val Asn	
190 195 200	
gac ggc ttt cag gct ctg caa ggc atc atc cac tca att ttg aag aag	797
Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys Lys	
205 210 215	
tcc tgc atc gaa att cta gca gct gaa cca tcc acc ata tgt gca gga	845
Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly	
220 225 230	
gag tca ttt caa gtt gtc gtg aga gga aac ggc ttc cga cat gcc cgc	893
Glu Ser Phe Gln Val Val Val Arg Gly Asn Gly Phe Arg His Ala Arg	
235 240 245 250	
aac gtg gac agg gtc ctc tgc agc ttc aag atc aat gac tcg gtc aca	941
Asn Val Asp Arg Val Leu Cys Ser Phe Lys Ile Asn Asp Ser Val Thr	
255 260 265	
ctc aat gag aag ccc ttt tct gtg gaa gat act tat tta ctg tgt cca	989
Leu Asn Glu Lys Pro Phe Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro	
270 275 280	

gcg cct atc tta aaa gaa gtt ggc atg aaa gct gca ctc cag gtc agc	1037
Ala Pro Ile Leu Lys Glu Val Gly Met Lys Ala Ala Leu Gln Val Ser	
285 290 295	
atg aac gat ggc ctc tct ttt atc tcc agt tct gtc atc atc acc acc	1085
Met Asn Asp Gly Leu Ser Phe Ile Ser Ser Ser Val Ile Ile Thr Thr	
300 305 310	
aca cac tgt tct gac ggt tcc atc ctg gcc atc gcc ctg ctg atc ctg	1133
Thr His Cys Ser Asp Gly Ser Ile Leu Ala Ile Ala Leu Leu Ile Leu	
315 320 325 330	
ttc ctg ctc cta gcc ctg gct ctc ctc tgg tgg ttc tgg ccc ctc tgc	1181
Phe Leu Leu Leu Ala Leu Ala Leu Leu Trp Trp Phe Trp Pro Leu Cys	
335 340 345	
tgc act gtg att atc aag gag gtc cct cca ccc cct gcc gag gag agt	1229
Cys Thr Val Ile Ile Lys Glu Val Pro Pro Pro Pro Ala Glu Glu Ser	
350 355 360	
gag gaa gaa gat gat gat ggt ctg cct aag aaa aag tgg cca acg gta	1277
Glu Glu Glu Asp Asp Asp Gly Leu Pro Lys Lys Lys Trp Pro Thr Val	
365 370 375	
gac gcc tct tat tat ggt ggg aga ggc gtt gga ggc att aaa aga atg	1325
Asp Ala Ser Tyr Tyr Gly Gly Arg Gly Val Gly Gly Ile Lys Arg Met	
380 385 390	
gag gtt cgt tgg gga gaa aag ggc tcc aca gaa gaa ggt gct aag ttg	1373
Glu Val Arg Trp Gly Glu Lys Gly Ser Thr Glu Glu Gly Ala Lys Leu	
395 400 405 410	
gaa aag gca aag aat gca aga gtc aag atg ccg gag cag gaa tat gaa	1421
Glu Lys Ala Lys Asn Ala Arg Val Lys Met Pro Glu Gln Glu Tyr Glu	
415 420 425	
ttc cct gag ccg cga aat ctc aac aac aat atg cgt cgg cct tct tcc	1469
Phe Pro Glu Pro Arg Asn Leu Asn Asn Asn Met Arg Arg Pro Ser Ser	
430 435 440	
ccc cgg aag tgg tac tct cca atc aag gga aaa ctc gat gcc ttg tgg	1517
Pro Arg Lys Trp Tyr Ser Pro Ile Lys Gly Lys Leu Asp Ala Leu Trp	
445 450 455	
gtc cta ctg agg aaa gga tat gat cgt gtg tct gtg atg cgt cca cag	1565
Val Leu Leu Arg Lys Gly Tyr Asp Arg Val Ser Val Met Arg Pro Gln	
460 465 470	
cca gga gac acg ggg cgc tgc atc aac ttc acc agg gtc aag aac aac	1613
Pro Gly Asp Thr Gly Arg Cys Ile Asn Phe Thr Arg Val Lys Asn Asn	
475 480 485 490	
cag cca gcc aag tac cca ctc aac aac gcc tac cac acc tcc tcg ccg	1661
Gln Pro Ala Lys Tyr Pro Leu Asn Asn Ala Tyr His Thr Ser Ser Pro	
495 500 505	



cct cct gcc ccc atc tac act ccc cca cct cct gcg ccc cac tgc cct 1709  
Pro Pro Ala Pro Ile Tyr Thr Pro Pro Pro Pro Ala Pro His Cys Pro  
510 515 520

ccc ccg ccc ccc agc gcc cct acc cct ccc atc ccg tcc cca cct tcc 1757  
Pro Pro Pro Pro Ser Ala Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser  
525 530 535

acc ctt ccc cct cct ccc cag gct cca cct ccc aac agg gca cct cct 1805  
Thr Leu Pro Pro Pro Pro Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro  
540 545 550

ccc tcc cgc cct cct cca agg cct tct gtc tagagcccaa agttcctgct 1855  
Pro Ser Arg Pro Pro Pro Arg Pro Ser Val  
555 560

ctgggctctc tcagaaactt caggagatgt tagaacaagt ctttccagtt agagaagagg 1915  
agtgggtgata aagccctactg accttcacac attctaaaaa ttggttgcca atgccagtat 1975  
accaacaatc atgatcagct gaaagaaaca gatattttta attgccagaa aacaaatgat 2035  
gaggcaacta cagtcagatt tatagccagc catctatcac ctctagaagg ttccagagac 2095  
agtgaaactg caagatgctc tcaacaggat tatgtctcat ggagaccagt aagaaaatca 2155  
tttatctgaa ggtgaaatgc agagttggat aagaaatata ttgctggggt tctaaaatgc 2215  
tgccttctcg cctctactcc acctccatcc ctggactttg gacccttggc ctaggagcct 2275  
aaggaccttc acccctgtgc accacccaag aaagaggaaa actttgccta caactttgga 2335  
aatgctgggg tccctgggtg ggtaagaaac tcaacatcag acgggtatgc agaaggatgt 2395  
tcttctggga tttgcaggta cataaaaaat gtatggcatc tttccttgc aaattcttcc 2455  
agtttccaag tgagaagggg agcagggtgt tactgatgga aaaggatatgt tgctatgttg 2515  
atgtgtaagt gaaatcagtt gtgtgcaata gacaggggcg tattcatggg agcatcagcc 2575  
agtttctaaa acccacaggc catcagcagc tagagggtggc tggctttggc cagacatgga 2635  
ccctaaatca acagacaatg gcattgtcga agagcaacct gttaatgaat catgttaaaa 2695  
atcaaggttt ggcttcagtt taaatcactt gaggtatgaa gtttatcctg ttttccagag 2755  
ataaacataa gttgatcttc ccaaaatacc atcattagga cctatcacac aatatcacta 2815  
gttttttttg tttgtttgtt tttgttttt tttcttggtg aagccatgca ccacagactt 2875  
ctgggcagag ctgagagaca atggtcctga cataataagg atctttgatt aacccccata 2935  
aggcatgtgt gtgtatacaa atatacttct ctttggcttt tcgacataga acctcagctg 2995  
ttaaccaagg ggaaatacat cagatctgca acacagaaat gctctgcctg aaatttccac 3055  
catgcctagg actcacccca tttatccagg tctttctgga tctgtttaat caataagccc 3115

tataatcact tgctaaacac tgggcttcat cccccagga taaaaacaga gatcattgtc 3175  
 ttggacctcc tgcacagcc tattcaaaat tatctctctc tctagctttc cacaaatcct 3235  
 aaaattcctg tccaagcca cccaaattct cagatctttt ctggaacaag gcagaatata 3295  
 aaataaatat acatttagtg gcttgggcta tgggtctcaa agatccttca aaaatacatc 3355  
 aagccagctt cattcactca ctttacttag aacagagata taagggcctg ggatgcattt 3415  
 attttatcaa taccaatttt tgtggccatg gcagacattg ctaatcaatc acagcactat 3475  
 ttctatttaa gccactgat ttcttcacaa tocttctcaa attacaattc caaagagccg 3535  
 ccactcaaca gtcagatgaa cccaacagtc agatgagaga aatgaaccct acttgctatc 3595  
 tctatcttag aaagcaaaaa caaacaggag ttccagga gaatgggaaa gccagggggc 3655  
 ataaaaggta cagtcagggg aaaatagatc taggcagagt gccttagtca gggaccacgg 3715  
 gcgctgaatc tgcagtgcc aacacaaact gacacatctc cagggtgtacc tccaacccta 3775  
 gccttctccc acagctgcct acaacagagt ctcccagcct tctcagagag ctaaaaccag 3835  
 aaatttccag actcatgaaa gcaaccccc agcctctccc caaccctgcc gcattgtcta 3895  
 atttttagaa cactaggctt cttctttcat gtagttctc ataagcaggg gccagaatat 3955  
 ctcagccacc tgcagtgaca ttgctggacc cctgaaaacc attccatagg agaatgggtt 4015  
 ccccaggtc acagtgtaga gacattgagc ccatcacaa tgttttgact gctggcagtc 4075  
 taaaacagtc ccccccccc atggcactgc cgcgtgattc ccgcggccat tcagaagttc 4135  
 aagccgagat gctgacgttg ctgagcaacg agatgggtgag catcagtgc aatgcaccat 4195  
 tcagcacatc agtcatatgc ccagtgcagt tacaagatgt tgtttcggca aagcattttg 4255  
 atggaatagg gaactgcaaa tgtatgatga ttttgaaaag gctcagcagg atttgttctt 4315  
 aaaccgactc agtgtgtcat ccccggttat ttagaattac agttaagaag gagaaacttc 4375  
 tataagactg tatgaacaag gtgatatctt catagtgggc tattacaggc aggaaaatgt 4435  
 tttaactggt ttacaaaatc catcaatact tgtgtcattc cctgtaaaag gcaggagaca 4495  
 tgtgattatg atcaggaaac tgcacaaaat tattgttttc agccccctg ttattgtcct 4555  
 tttgaactgt ttttttttta ttaaagccaa atttgtgttg tatatattcg tattccatgt 4615  
 gttagatgga agcatttcct atccagtgtg aataaaaaga acagttgtag taaattatta 4675  
 taaagccgat gatatttcat ggcagggttat tctaccaagc tgtgcttggt gggttttccc 4735  
 atgactgtat tgcttttata aatgtacaaa tagttactga aatgacgaga cccttggttg 4795

cacagcatta ataagaacct tgataagaac catattctgt tgacagccag ctcacagttt 4855  
 cttgcctgaa gcttggtgca ccctccagt agacacaaga tctctctttt accaaagttg 4915  
 agaacagagc tgggtggatta attaatagtc ttcgatatct ggccatgggt aacctcattg 4975  
 taactatcat cagaatgggc agagatgata ttgaagtgtc acatacacta aagtccaaac 5035  
 actatgtcag atgggggtaa aatccattaa agaacaggaa aaaataatta taagatgata 5095  
 agcaaagtgt tcagcccaat gtcaaccag ttaaaaaaaaa aattaatgct gtgtaaaatg 5155  
 gttgaattag tttgcaaact atataaagac atatgcagta aaaagtctgt taatgcacat 5215  
 cctgtgggaa tggagtgttc taaccaattg ccttttcttg ttatctgagc tctctatat 5275  
 tatcatactc agataaccaa attaaaagaa ttagaatatg atttttaata cacttaacat 5335  
 taaactcttc taactttctt ctttctgtga taattcagaa gatagttatg gatcttcaat 5395  
 gcctctgagt cattgttata aaaaatcagt tatcactata ccatgctata ggagactggg 5455  
 caaaacctgt acaatgacaa ccctggaagt tgcttttttt aaaaaataa taaatttctt 5515  
 aaatcaaaaa aaaaaaaaaa aaaaa 5540

<210> 6

<211> 564

<212> PRT

<213> Homo sapiens

<400> 6

Met Ala Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu  
 1 5 10 15

Ser Leu Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg  
 20 25 30

Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile  
 35 40 45

Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr  
 50 55 60

Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met  
 65 70 75 80

Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr  
 85 90 95

Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val  
 100 105 110

Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser  
 115 120 125



Leu Asn Asn Asn Met Arg Arg Pro Ser Ser Pro Arg Lys Trp Tyr Ser  
 435 440 445  
 Pro Ile Lys Gly Lys Leu Asp Ala Leu Trp Val Leu Leu Arg Lys Gly  
 450 455 460  
 Tyr Asp Arg Val Ser Val Met Arg Pro Gln Pro Gly Asp Thr Gly Arg  
 465 470 475 480  
 Cys Ile Asn Phe Thr Arg Val Lys Asn Asn Gln Pro Ala Lys Tyr Pro  
 485 490 495  
 Leu Asn Asn Ala Tyr His Thr Ser Ser Pro Pro Pro Ala Pro Ile Tyr  
 500 505 510  
 Thr Pro Pro Pro Pro Ala Pro His Cys Pro Pro Pro Pro Pro Ser Ala  
 515 520 525  
 Pro Thr Pro Pro Ile Pro Ser Pro Pro Ser Thr Leu Pro Pro Pro Pro  
 530 535 540  
 Gln Ala Pro Pro Pro Asn Arg Ala Pro Pro Pro Ser Arg Pro Pro Pro  
 545 550 555 560  
 Arg Pro Ser Val

<210> 7  
 <211> 2112  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (113)..(1111)

<400> 7  
 ggggaataaa ggacccgcga ggaagggccc gcggatggcg cgtccctgag ggtcgtggcg 60  
 agttcgcgga gcgtgggaag gagcggaccc tgcctcctccc gggctgcggg cc atg gcc 118  
 Met Ala  
 1

acg gcg gag cgg aga gcc ctc ggc atc ggc ttc cag tgg ctc tct ttg 166  
 Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu Ser Leu  
 5 10 15

gcc act ctg gtg ctc atc tgc gcc ggg caa ggg gga cgc agg gag gat 214  
 Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Arg Arg Glu Asp  
 20 25 30

ggg ggt cca gcc tgc tac ggc gga ttt gac ctg tac ttc att ttg gac 262  
 Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile Leu Asp  
 35 40 45 50

aaa tca gga agt gtg ctg cac cac tgg aat gaa atc tat tac ttt gtg	310
Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr Phe Val	
55 60 65	
gaa cag ttg gct cac aaa ttc atc agc cca cag ttg aga atg tcc ttt	358
Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met Ser Phe	
70 75 80	
att gtt ttc tcc acc cga gga aca acc tta atg aaa ctg aca gaa gac	406
Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr Glu Asp	
85 90 95	
aga gaa caa atc cgt caa ggc cta gaa gaa ctc cag aaa gtt ctg cca	454
Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val Leu Pro	
100 105 110	
gga gga gac act tac atg cat gaa gga ttt gaa agg gcc agt gag cag	502
Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser Glu Gln	
115 120 125 130	
att tat tat gaa aac aga caa ggg tac agg aca gcc agc gtc atc att	550
Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val Ile Ile	
135 140 145	
gct ttg act gat gga gaa ctc cat gaa gat ctc ttt ttc tat tca gag	598
Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr Ser Glu	
150 155 160	
agg gag gct aat agg tct cga gat ctt ggt gca att gtt tac tgt gtt	646
Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr Cys Val	
165 170 175	
ggt gtg aaa gat ttc aat gag aca cag ctg gcc cgg att gcg gac agt	694
Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala Asp Ser	
180 185 190	
aag gat cat gtg ttt ccc gtg aat gac ggc ttt cag gct ctg caa ggc	742
Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu Gln Gly	
195 200 205 210	
atc atc cac tca att ttg aag aag tcc tgc atc gaa att cta gca gct	790
Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu Ala Ala	
215 220 225	
gaa cca tcc acc ata tgt gca gga gag tca ttt caa gtt gtc gtg aga	838
Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val Val Arg	
230 235 240	
gga aac ggc ttc cga cat gcc cgc aac gtg gac agg gtc ctc tgc agc	886
Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu Cys Ser	
245 250 255	
ttc aag atc aat gac tgc gtc aca ctc aat gag aag ccc ttt tct gtg	934
Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe Ser Val	
260 265 270	

gaa gat act tat tta ctg tgt cca gcg cct atc tta aaa gaa gtt ggc 982  
 Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu Val Gly  
 275 280 285 290  
  
 atg aaa gct gca ctc cag gtc agc atg aac gat ggc ctc tct ttt atc 1030  
 Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser Phe Ile  
 295 300 305  
  
 tcc agt tct gtc atc atc acc acc aca cac tgt agc ctc cac aaa att 1078  
 Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Leu His Lys Ile  
 310 315 320  
  
 gca tca ggc ccc aca aca gct gct tgc atg gaa tagcagagaa taccgcctgc 1131  
 Ala Ser Gly Pro Thr Thr Ala Ala Cys Met Glu  
 325 330  
  
 tccctccgga cagcacactc ctgaaaacgg ggagagagga gccaaacatg ctcggtttac 1191  
 actttcctta tttactgaat gagtggaggg cagagacagg cctggagtta cgcacactga 1251  
 gtgccccaac atggaaagaa acatcaggag ggacaggaaa cgttccctcc ttaaccaaca 1311  
 gttttcaaga ccttactgga ggcactttat tggctacata atcaactccat gcggtgggca 1371  
 tcaggcagaa tcctggtgca gacccaactt tgaggtggag gatttcacag tttctttatt 1431  
 ttgaacttcc cccaggctcc cactaattcc tctccattct atcctoctcc ctttcccaca 1491  
 aaagaaaaca gaaaggagca gcagtgttg ataccgtatc atccagaggc ctggttctct 1551  
 cccattatag ggcaacaag ccttggaag atatttcact cccgccccat gccatgcatt 1611  
 aaaaatccaa aattgcctat attccacctg ccaagcaaga gatgctttca ttattgaagt 1671  
 tccaaatgta tacctttgag aacagtgcct tctcgtctta aaagagaggt cctcattttg 1731  
 tgagttggga gcagagggaa ttaaagaaag ccatgatgca gggatttggc cattcaagcc 1791  
 gggcagcctt cagagaatgt catcccta atacacatgcc cgaatgaagg agcggggctg 1851  
 agcttgtcct gccttcgtat tgaatgttgc ctgtctgcct ccttaatagc gggcctctgt 1911  
 gtgagcattt gacaagactt aaaactattc attgaagaaa atggatgatc ccccaacagg 1971  
 aagatgcaac cccatgggct gcctgcttga ccacagaagt gcttcagct ccagttgctc 2031  
 atctgagaac tccccccacc acttgcgtgtt aaaattgtta aaattaaagg ccatgttgat 2091  
 tgaaaaaaaa aaaaaaaaaa a 2112

<210> 8

<211> 333

<212> PRT

<213> Homo sapiens

<400> 8

Met Ala Thr Ala Glu Arg Arg Ala Leu Gly Ile Gly Phe Gln Trp Leu  
 1 5 10 15  
 Ser Leu Ala Thr Leu Val Leu Ile Cys Ala Gly Gln Gly Gly Arg Arg  
 20 25 30  
 Glu Asp Gly Gly Pro Ala Cys Tyr Gly Gly Phe Asp Leu Tyr Phe Ile  
 35 40 45  
 Leu Asp Lys Ser Gly Ser Val Leu His His Trp Asn Glu Ile Tyr Tyr  
 50 55 60  
 Phe Val Glu Gln Leu Ala His Lys Phe Ile Ser Pro Gln Leu Arg Met  
 65 70 75 80  
 Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu Thr  
 85 90 95  
 Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys Val  
 100 105 110  
 Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala Ser  
 115 120 125  
 Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser Val  
 130 135 140  
 Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe Tyr  
 145 150 155 160  
 Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val Tyr  
 165 170 175  
 Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile Ala  
 180 185 190  
 Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala Leu  
 195 200 205  
 Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile Leu  
 210 215 220  
 Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val Val  
 225 230 235 240  
 Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val Leu  
 245 250 255  
 Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Asn Glu Lys Pro Phe  
 260 265 270  
 Ser Val Glu Asp Thr Tyr Leu Leu Cys Pro Ala Pro Ile Leu Lys Glu  
 275 280 285  
 Val Gly Met Lys Ala Ala Leu Gln Val Ser Met Asn Asp Gly Leu Ser  
 290 295 300



Phe Ile Ser Ser Ser Val Ile Ile Thr Thr Thr His Cys Ser Leu His  
305 310 315 320

Lys Ile Ala Ser Gly Pro Thr Thr Ala Ala Cys Met Glu  
325 330

<210> 9

<211> 1436

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (380)..(1033)

<400> 9

aattgcttcc ggggagttgc gagggagcga gggggaataa aggacccgcg aggaagggcc 60

cgcggatggc gcgtccctga gggtcgtggc gagttcgcgg agcgtgggaa ggagcggacc 120

ctgctctccc cgggctgcgg gccatggcca cggcggagcg gagagccctc ggcacggtct 180

tccagtggct ctcacggcca ctctggtgct catctgcgcc gggcaagggg gacgcaggga 240

ggatgggggt ccagcctgct acggcggatt tgacctgtac ttcattttgg acaaatcagg 300

aagtgtgctg caccactgga atgaaatcta ttactttgtg gaacagttgg ctacaaaatt 360

catcagccca cagttgaga atg tcc ttt att gtt ttc tcc acc cga gga aca 412

Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr  
1 5 10

acc tta atg aaa ctg aca gaa gac aga gaa caa atc cgt caa ggc cta 460

Thr Leu Met Lys Leu Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu  
15 20 25

gaa gaa ctc cag aaa gtt ctg cca gga gga gac act tac atg cat gaa 508

Glu Glu Leu Gln Lys Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu  
30 35 40

gga ttt gaa agg gcc agt gag cag att tat tat gaa aac aga caa ggg 556

Gly Phe Glu Arg Ala Ser Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly  
45 50 55

tac agg aca gct agc gtc atc att gct ttg act gat gga gaa ctc cat 604

Tyr Arg Thr Ala Ser Val Ile Ile Ala Leu Thr Asp Gly Glu Leu His  
60 65 70 75

gaa gat ctc ttt ttc tat tca gag agg gag gct aat agg tct cga gat 652

Glu Asp Leu Phe Phe Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp  
80 85 90

ctt ggt gca att gtt tac tgt gtt ggt gtg aaa gat ttc aat gag aca 700

Leu Gly Ala Ile Val Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr  
95 100 105

cag ctg gcc cgg att gcg gac agt aag gat cat gtg ttt ccc gtg aat 748  
 Gln Leu Ala Arg Ile Ala Asp Ser Lys Asp His Val Phe Pro Val Asn  
 110 115 120

gac ggc ttt cag gct ctg caa ggc atc atc cac tca att ttg aag aag 796  
 Asp Gly Phe Gln Ala Leu Gln Gly Ile Ile His Ser Ile Leu Lys Lys  
 125 130 135

tcc tgc atc gaa att cta gca gct gaa cca tcc acc ata tgt gca gga 844  
 Ser Cys Ile Glu Ile Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly  
 140 145 150 155

gag tca ttt caa gtt gtc gtg aga gga aac ggc ttc cga cat gcc cgc 892  
 Glu Ser Phe Gln Val Val Val Arg Gly Asn Gly Phe Arg His Ala Arg  
 160 165 170

aac gtg gac agg gtc ctc tgc agc ttc aag atc aat gac tcg gtc aca 940  
 Asn Val Asp Arg Val Leu Cys Ser Phe Lys Ile Asn Asp Ser Val Thr  
 175 180 185

ctc agt aag tcc ttg cag agt cca tgg gtt tct tcg aca agt ggc ttc 988  
 Leu Ser Lys Ser Leu Gln Ser Pro Trp Val Ser Ser Thr Ser Gly Phe  
 190 195 200

aag gaa ggg aat tcc cac cct tgt ctt cca gca agg cca cac aca 1033  
 Lys Glu Gly Asn Ser His Pro Cys Leu Pro Ala Arg Pro His Thr  
 205 210 215

tgaaaccagc agaaaagagt cttatttgct ggaaagaccc ccagcaaggg catagtgagc 1093

ccttacagtg gttccagtca gaaaaggcac cacttgggtg ggcacagccc catgggtgtc 1153

caacttggtg agcagagcaa ggctggactt gagtccccgt cctccacaaa acacagagcc 1213

acaagcccca gccctgcagc agccctccgg aagcagcggg gcactgggtt ccttgtcccc 1273

tgccatctac cgagtggctc actctcaggt gggagtgtg gtgatgggta attaggactg 1333

cagaaacatg agcctcctta acaaagtatt gggactctta agggtaagtg tgaaaaagga 1393

atggtctaaa tgcattaatc ttgaataaac cgaaaaccaa acc 1436

<210> 10

<211> 218

<212> PRT

<213> Homo sapiens

<400> 10

Met Ser Phe Ile Val Phe Ser Thr Arg Gly Thr Thr Leu Met Lys Leu  
 1 5 10 15

Thr Glu Asp Arg Glu Gln Ile Arg Gln Gly Leu Glu Glu Leu Gln Lys  
 20 25 30

Val Leu Pro Gly Gly Asp Thr Tyr Met His Glu Gly Phe Glu Arg Ala  
 35 40 45  
 Ser Glu Gln Ile Tyr Tyr Glu Asn Arg Gln Gly Tyr Arg Thr Ala Ser  
 50 55 60  
 Val Ile Ile Ala Leu Thr Asp Gly Glu Leu His Glu Asp Leu Phe Phe  
 65 70 75 80  
 Tyr Ser Glu Arg Glu Ala Asn Arg Ser Arg Asp Leu Gly Ala Ile Val  
 85 90 95  
 Tyr Cys Val Gly Val Lys Asp Phe Asn Glu Thr Gln Leu Ala Arg Ile  
 100 105 110  
 Ala Asp Ser Lys Asp His Val Phe Pro Val Asn Asp Gly Phe Gln Ala  
 115 120 125  
 Leu Gln Gly Ile Ile His Ser Ile Leu Lys Lys Ser Cys Ile Glu Ile  
 130 135 140  
 Leu Ala Ala Glu Pro Ser Thr Ile Cys Ala Gly Glu Ser Phe Gln Val  
 145 150 155 160  
 Val Val Arg Gly Asn Gly Phe Arg His Ala Arg Asn Val Asp Arg Val  
 165 170 175  
 Leu Cys Ser Phe Lys Ile Asn Asp Ser Val Thr Leu Ser Lys Ser Leu  
 180 185 190  
 Gln Ser Pro Trp Val Ser Ser Thr Ser Gly Phe Lys Glu Gly Asn Ser  
 195 200 205  
 His Pro Cys Leu Pro Ala Arg Pro His Thr  
 210 215